

REPLACEMENT SHEET

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FIGURE 1A

1 atggcccaag cccctgcctg gctcctgctg tggatgggag cgggagtgct
51 gcttgcctcc agcccccagc cccgcatccg gctgcctctg cgcagcggcc
101 tgggggggccc ccccttgggg ctggggctgg cccgggagac cgaagagag
151 cccgaggagc cgggcgggag gggcagcttc gtggagatgg tggacacac
201 gagggggagc tgggggagc gctactactg gggatganc gtggggcagc
251 cccggcagac gctcaccacc ctggtgggata cgggcagcag taactttgca
301 gtgggtgctg ccccccaccc cttcctgcat cgtactaac agaggcagct
351 gtccagcaca tccgggggac tccgggaagg tgtgtatgtg cctacaccc
401 cgggcaagtg ggaaggggag ctggggcacc acctggtaag cctccccc
451 gggcccccacg tccctgtggg tgcacacatt gctgcctcca ctgaatcaga
501 caagtctctc atccacgggt ccaactggga aggcaccccg gggctggct
551 atgctgagat tggcaggatc attggaggta tgcaccctc gctgtacac
601 ggcagctctc ggtatacacc cctccggggg ggtgggtatt atgaggtcat
651 catgtgtggg ggggagatca atggacagga tctgaaatg gscgtcaagg
701 agtccaccta tgcacagagc attgtggaca ggggcacac caaccttcgt
751 ttgcccagga aagtgtttga aggtgcagtc aaatccatca aggaagcctc
801 ctcacgggag aagttccctg atgggtctct gctaggagag cagctgggtg
851 gctggcagag aggcacaccc ccttgggaaca ttttccagct cctccctc
901 taccataatg gtgagggtac caaccagtc tccgcacat caatccctcc
951 gcagcaatac ctgcccggag tgggaagatg ggcacagtc caagaagact
1001 gttcacaagt tgcacatcca cagtcaccca cgggcactgt tatgggagct
1051 gttatcatgg agggcttcca cgttgtcttt gctcgggccc gaaacgaat
1101 tgggtttgct gtcagcgctt gccatgtgca cgtatgagtc aggaagcgag
1151 cgggtggaag cccctttgtc acctgggaca tgggaagctg tgggtacac
1201 attccacaga cagatgagtc aacctcatg accatagcct atgtcatggc
1251 tgcacatctg gccctctcca tgcctgcact ctgctcatg gtgtgtcagt
1301 ggcgctgct cccgtgcctg cgcagcagc atgatgact tgcgtatgac
1351 atctccctgc tgaagtga

FIGURE 1B

BACE501: 1 MAQALFWLLWNGGVLPARGTQNGIRLPLRSGLGGAFLGLRLPRETDEEPPEPGRGSP 60
MAQALFWLLWNGGVLPARGTQNGIRLPLRSGLGGAFLGLRLPRETDEEPPEPGRGSP
BACE455: 1 MAQALFWLLWNGGVLPARGTQNGIRLPLRSGLGGAFLGLRLPRETDEEPPEPGRGSP 60
BACE501: 61 VEMVDNLPGHSGQYYVEMTVGSPPTLNI LVLTGSSNFVGAAPHFLHRYTQRLSST 120
VEMVDNLPGHSGQYYVEMTVGSPPTLNI LVLTGSSNFVGAAPHFLHRYTQRLSST
BACE455: 61 VEMVDNLPGHSGQYYVEMTVGSPPTLNI LVLTGSSNFVGAAPHFLHRYTQRLSST 120
BACE501: 121 YKDLRFQVYVPTQGRWEGELGTDLVSI PHGPNVTVRANTAAITSDKPFINGSNWEGIL 180
YKDLRFQVYVPTQGRWEGELGTDLVSI PHGPNVTVRANTAAITSDKPFINGSNWEGIL
BACE455: 121 YKDLRFQVYVPTQGRWEGELGTDLVSI PHGPNVTVRANTAAITSDKPFINGSNWEGIL 180
BACE501: 181 GLAYARIARPDOSLEPFPU3LVKQTHVPLNLSGLQCGAGWPLNQSEVLASVGTSMIGGI 240
GLAYARIARPDOSLEPFPU3LVKQTHVPLNLSGLQCGAGWPLNQSEVLASVGTSMIGGI
BACE455: 181 GLAYARIARPDOSLEPFPU3LVKQTHVPLNLSGLQCGAGWPLNQSEVLASVGTSMIGGI 240
BACE501: 241 DHSLYTGSLSWTPI RREWYIEVI IVRVBINGQDLMDCKEYNYDKS IVDGTTNLRLPKK 300
DHSLYTGSLSWTPI RREWYIEVI IVRVBINGQDLMDCKEYNYDKS IVDGTTNLRLPKK
BACE455: 241 DHSLYTGSLSWTPI RREWYIEVI IVRVBINGQDLMDCKEYNYDKS IVDGTTNLRLPKK 300
BACE501: 301 VFPAAYKSIKASSTKFPDGFPLGQLVCWQAGTTFWNI FVVISLXLMGEVTVNQSPRIT 360
VFPAAYKSIKASSTKFPDGFPLGQLVCWQAGTTFWNI FVVISLXLMGEVTVNQSPRIT
BACE455: 301 VFPAAYKSIKASSTKFPDGFPLGQLVCWQAGTTFWNI FVVISLXLMGEVTVNQSPRIT 360
BACE501: 361 ILPQQYLRFVBDVATSGDDCYKFAISQSSTGTVMGAVIMEGFYVVFDPARKRI GFPAVSAC 420
ILPQQYLRFVBDVATSGDDCYKFAISQSSTGTVMGAVIMEGFYVVFDPARKRI GFPAVSAC
BACE455: 361 ILPQQYLRFVBDVATSGDDCYKFAISQSSTGTVMGAVIMEGFYVVFDPARKRI GFPAVSAC 420
BACE501: 421 HVHDEFRTAAVEGPFVTLDMEDCGYNI PQTDSTLMTIAYVMAALCALFMLPLCLMVCCW 480
HVHDEFRTAAVEGPFVTLDMEDCGYNI PQTDSTLMTIAYVMAALCALFMLPLCLMVCCW
BACE455: 421 HVHDEFRTAAVEGPFVTLDMEDCGYNI PQTDSTLMTIAYVMAALCALFMLPLCLMVCCW 480
BACE501: 481 RCLRCLRQKHODFADDISLLK 501
RCLRCLRQKHODFADDISLLK
BACE455: 481 RCLRCLRQKHODFADDISLLK 501

REPLACEMENT SHEET

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FIGURE 2A

FIGURE 2B

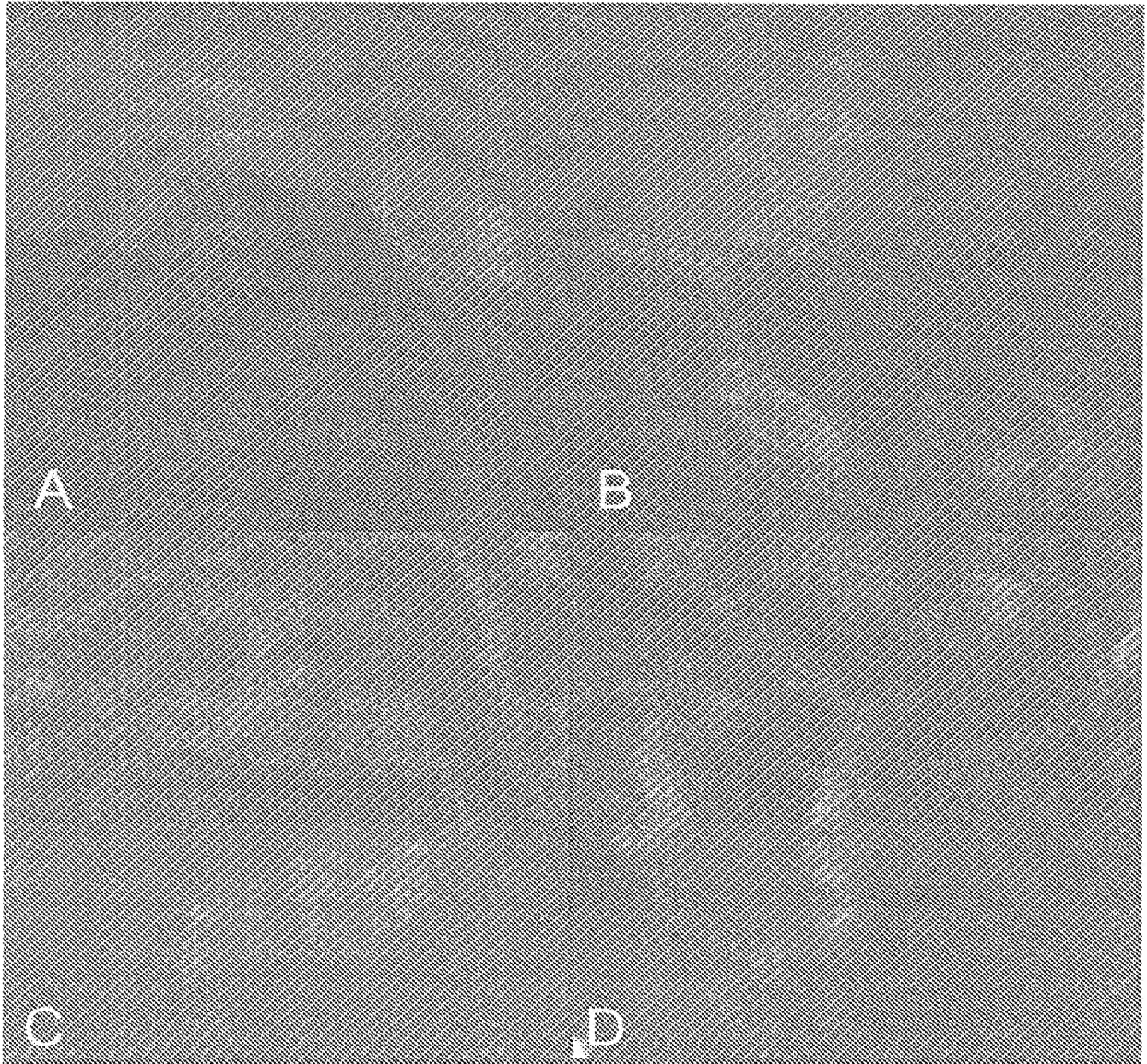


FIGURE 2C

FIGURE 2D

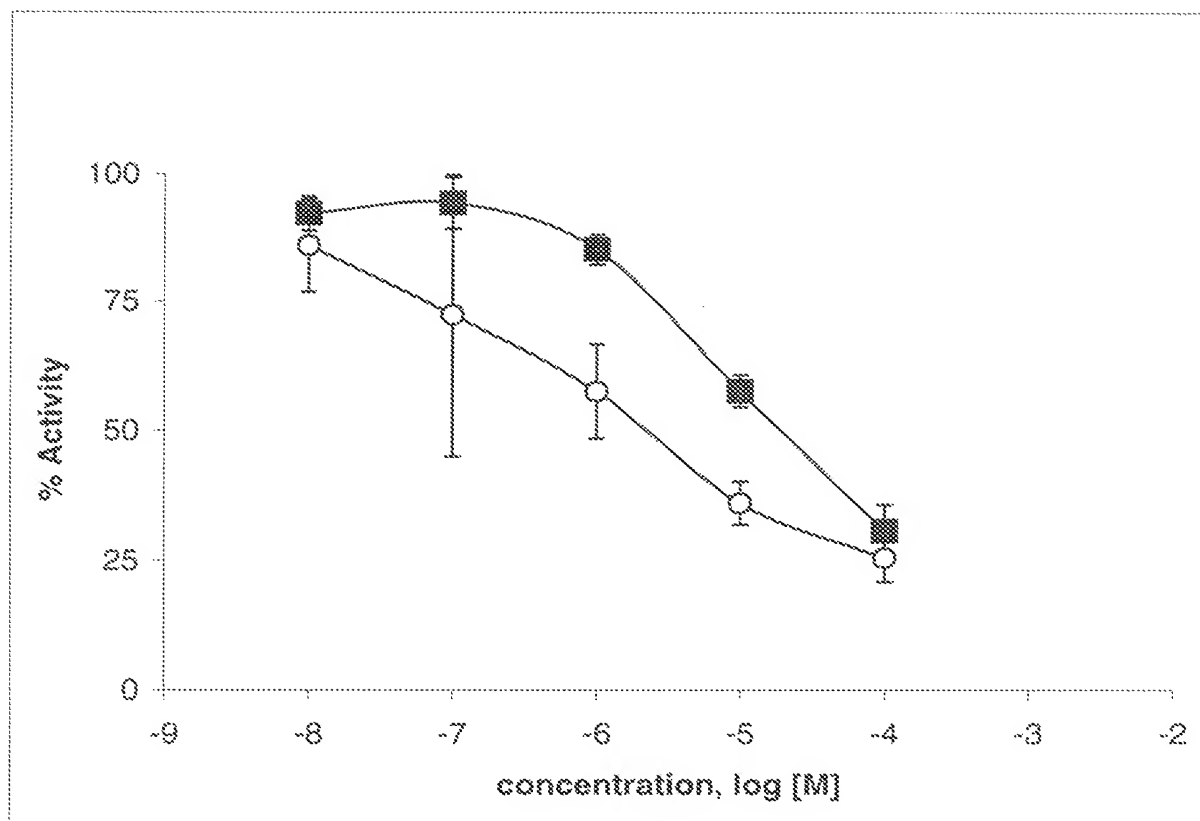


Figure 3

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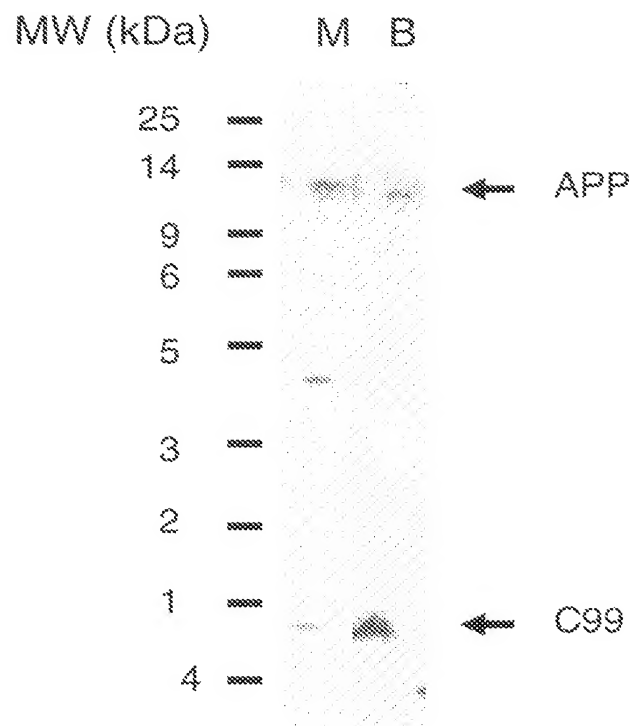


Figure 4

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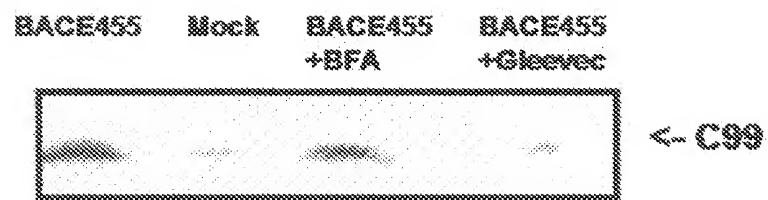


Figure 5